SEQUENCE LISTING

DNASIS DNA Translation [T-INS]
File Name : T-INS
Range :   2 -   7286   Mode : Normal
Codon Table : Universal

(handwritten: start of SEQ 3 + 4)

```
                10           19           28           37           46           55
5'  GAG CTG AGC TGA ACT GGC CCT CCT GGG GAC TCA GCA AGC TCT CTA GAG CCC CCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     E   L   S   *   T   G   P   P   G   D   S   A   S   S   L   E   P   P

                64           73           82           91          100          109
    ACA TGC TCC CCC ACC GGG GTC CCC CGG TTG CGT GAG GAC ACC TCC TCT GAG GGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     T   C   S   P   T   G   V   P   R   L   R   E   D   T   S   S   E   G

                118          127          136          145          154          163
    CTC CGC TCG CCC CTC TTC GGA CCC CCC GGG GCC CCG GCT GGC CAG AGG ATG GAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   R   S   P   L   F   G   P   P   G   A   P   A   G   Q   R   M   D

                172          181          190          199          208          217
    GAG GAG GAG GAT GGA GCG GGC GCC GAG GAG TCG GGA CAG CCC CGT AGC TTC ACG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     E   E   E   D   G   A   G   A   E   E   S   G   Q   P   R   S   F   T

                226          235          244          253          262          271
    CAG CTC AAC GAC CTG TCC GGG GCC GGG GGC CGG CAG GGG CCG GGG TCG ACG GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Q   L   N   D   L   S   G   A   G   R   Q   G   P   G   S   T   E

                280          289          298          307          316          325
    AAG GAC CCG GGC AGC GCG GAC TCC GAG GCG GAG GGG CTG CCG TAC CCG GCG CTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     K   D   P   G   S   A   D   S   E   A   E   G   L   P   Y   P   A   L

                334          343          352          361          370          379
    GCC CCG GTG GTT TTC TTC TAC TTG AGC CAG GAC AGC CGC CCG CGG AGC TGG TGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   P   V   V   F   F   Y   L   S   Q   D   S   R   P   R   S   W   C

                388          397          406          415          424          433
    CTC CGC ACG GTC TGT AAC CCG TGG TTC GAG CGA GTC AGT ATG CTG GTC ATT CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   R   T   V   C   N   P   W   F   E   R   V   S   M   L   V   I   L

                442          451          460          469          478          487
    CTC AAC TGT GTG ACT CTG GGT ATG TTC AGG CCG TGT GAG GAC ATT GCC TGT GAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   N   C   V   T   L   G   M   F   R   P   C   E   D   I   A   C   D

                496          505          514          523          532          541
    TCC CAG CGC TGC CGG ATC CTG CAG GCC TTC GAT GAC TTC ATC TTT GCC TTC TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     S   Q   R   C   R   I   L   Q   A   F   D   D   F   I   F   A   F   F

                550          559          568          577          586          595
    GCT GTG GAA ATG GTG GTG AAG ATG GTG GCC TTG GGC ATC TTT GGG AAG AAA TGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   V   E   M   V   V   K   M   V   A   L   G   I   F   G   K   K   C

                604          613          622          631          640          649
    TAC CTG GGA GAC ACT TGG AAC CGG CTT GAC TTT TTC ATT GTC ATT GCA GGG ATG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     Y   L   G   D   T   W   N   R   L   D   F   F   I   V   I   A   G   M
```

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DNASIS   DNA Translation [T-INS]

```
         658         667         676         685         694         703
CTG GAG TAT TCG CTG GAC CTG CAG AAC GTC AGC TTC TCC GCA GTC AGG ACA GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   Y   S   L   D   L   Q   N   V   S   F   S   A   V   R   T   V

         712         721         730         739         748         757
CGT GTG CTG CGA CCG GTC AGG GCC ATT AAC CGG GTG CCC AGC ATG CGC ATT CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   V   L   R   P   L   R   A   I   N   R   V   P   S   M   R   I   L

         766         775         784         793         802         811
GTC ACA TTA CTG CTG GAC ACC TTG CCT ATG CTG GGC AAC GTC CTG CTG CTC TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   T   L   L   L   D   T   L   P   M   L   G   N   V   L   L   L   C

         820         829         838         847         856         865
TTC TTC GTC TTT TTC ATC TTT GGC ATC GTG GGC GTC CAG CTG TGG GCA GGA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   F   V   F   F   I   F   G   I   V   G   V   Q   L   W   A   G   L

         874         883         892         901         910         919
CTT CGC AAC CGA TGC TTC CTC CCC GAG AAC TTC AGC CTC CCC CTG AGC GTG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   R   N   R   C   F   L   P   E   N   F   S   L   P   L   S   V   D

         928         937         946         955         964         973
CTG GAG CCT TAT TAC CAG ACA GAG AAT GAG GAC GAG AGC CCC TTC ATC TGC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   P   Y   Y   Q   T   E   N   E   D   E   S   P   F   I   C   S

         982         991        1000        1009        1018        1027
CAG CCT CGG GAG AAT GGC ATG AGA TCC TGC AGG AGT GTG CCC ACA CTG CGT GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   P   R   E   N   G   M   R   S   C   R   S   V   P   T   L   R   G

        1036        1045        1054        1063        1072        1081
GAA GGC GGT GGT GGC CCA CCC TGC AGT CTG GAC TAT GAG ACC TAT AAC AGT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   G   G   G   P   P   C   S   L   D   Y   E   T   Y   N   S   S

        1090        1099        1108        1117        1126        1135
AGC AAC ACC ACC TGT GTC AAC TGG AAC CAG TAC TAT ACC AAC TGC TCT GCG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   T   T   C   V   N   W   N   Q   Y   Y   T   N   C   S   A   G

        1144        1153        1162        1171        1180        1189
GAG CAC AAC CCC TTC AAA GGC GCC ATC AAC TTT GAC AAC ATT GGC TAT GCC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   H   N   P   F   K   G   A   I   N   F   D   N   I   G   Y   A   W

        1198        1207        1216        1225        1234        1243
ATC GCC ATC TTC CAG GTC ATC ACA CTG GAG GGC TGG GTC GAC ATC ATG TAC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   I   F   Q   V   I   T   L   E   G   W   V   D   I   M   Y   F

        1252        1261        1270        1279        1288        1297
GTA ATG GAC GCT CAC TCC TTC TAC AAC TTC ATC TAC TTC ATT CTT CTC ATC ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   M   D   A   H   S   F   Y   N   F   I   Y   F   I   L   L   I   I

        1306        1315        1324        1333        1342        1351
GTG GGC TCC TTC TTC ATG ATC AAC CTG TGC CTG GTG GTG ATT GCC ACG CAG TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   G   S   F   F   M   I   N   L   C   L   V   V   I   A   T   Q   F
```

DNASIS   DNA Translation [T-INS]

```
        1360       1369       1378       1387       1396       1405
TCC GAG ACC AAA CAG CGG GAG AGT CAG CTG ATG CGG GAG CAG CGT GTA CGA TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   E   T   K   Q   R   E   S   Q   L   M   R   E   Q   R   V   R   F

        1414       1423       1432       1441       1450       1459
CTG TCC AAT GCT AGC ACC CTG GCA AGC TTC TCT GAG CCA GGC AGC TGC TAT GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   S   N   A   S   T   L   A   S   F   S   E   P   G   S   C   Y   E

        1468       1477       1486       1495       1504       1513
GAG CTA CTC AAG TAC CTG GTG TAC ATC CTC CGA AAA GCA GCC CGA AGG CTG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   L   L   K   Y   L   V   Y   I   L   R   K   A   A   R   R   L   A

        1522       1531       1540       1549       1558       1567
CAG GTC TCT AGG GCT ATA GGC GTG CGG GCT GGG CTG CTC AGC AGC CCA GTG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   V   S   R   A   I   G   V   R   A   G   L   L   S   S   P   V   A

        1576       1585       1594       1603       1612       1621
CGT AGT GGG CAG GAG CCC CAG CCC AGT GGC AGC TGC ACT CGC TCA CAC CGT CGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   S   G   Q   E   P   Q   P   S   G   S   C   T   R   S   H   R   R

        1630       1639       1648       1657       1666       1675
CTG TCT GTC CAC CAC CTG GTC CAC CAC CAT CAC CAC CAC CAT CAC CAC TAC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   S   V   H   H   L   V   H   H   H   H   H   H   H   H   H   Y   H

        1684       1693       1702       1711       1720       1729
CTG GGT AAT GGG ACG CTC AGA GTT CCC CGG GCC AGC CCA GAG ATC CAG GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   G   N   G   T   L   R   V   P   R   A   S   P   E   I   Q   D   R

        1738       1747       1756       1765       1774       1783
GAT GCC AAT GGG TCT CGC CGG CTC ATG CTA CCA CCA CCC TCT ACA CCC ACT CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   A   N   G   S   R   R   L   M   L   P   P   P   S   T   P   T   P

        1792       1801       1810       1819       1828       1837
TCT GGG GGC CCT CCG AGG GGT GCG GAG TCT GTA CAC AGC TTC TAC CAT GCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   G   P   P   R   G   A   E   S   V   H   S   F   Y   H   A   D

        1846       1855       1864       1873       1882       1891
TGC CAC TTG GAG CCA GTC CGT TGC CAG GCA CCC CCT CCC AGA TGC CCA TCG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   H   L   E   P   V   R   C   Q   A   P   P   P   R   C   P   S   E

        1900       1909       1918       1927       1936       1945
GCA TCT GGT AGG ACT GTG GGT AGT GGG AAG GTG TAC CCC ACT GTG CAT ACC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   S   G   R   T   V   G   S   G   K   V   Y   P   T   V   H   T   S

        1954       1963       1972       1981       1990       1999
CCT CCA CCA GAG ATA CTG AAG GAT AAA GCA CTA GTG GAG GTG GCC CCC AGC CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   P   P   E   I   L   K   D   K   A   L   V   E   V   A   P   S   P

        2008       2017       2026       2035       2044       2053
GGG CCC CCC ACC CTC ACC AGC TTC AAC ATC CCA CCT GGG CCC TTC AGC TCC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   P   P   T   L   T   S   F   N   I   P   P   G   P   F   S   S   M
```

DNASIS   DNA Translation [T-INS]

```
          2062          2071          2080          2089          2098          2107
     CAC AAG CTC CTG GAG ACA CAG AGT ACG GGA GCC TGC CAT AGC TCC TGC AAA ATC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      H   K   L   L   E   T   Q   S   T   G   A   C   H   S   S   C   K   I

          2116          2125          2134          2143          2152          2161
     TCC AGC CCT TGC TCC AAG GCA GAC AGT GGA GCC TGC GGG CCG GAC AGT TGT CCC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      S   S   P   C   S   K   A   D   S   G   A   C   G   P   D   S   C   P

          2170          2179          2188          2197          2206          2215
     TAC TGT GCC CGG ACA GGA GCA GGA GAG CCA GAG TCC GCT GAC CAT GTC ATG CCT
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      Y   C   A   R   T   G   A   G   E   P   E   S   A   D   H   V   M   P

          2224          2233          2242          2251          2260          2269
     GAC TCA GAC AGC GAG GCT GTG TAT GAG TTC ACA CAG GAC GCT CAG CAC AGT GAC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      D   S   D   S   E   A   V   Y   E   F   T   Q   D   A   Q   H   S   D

          2278          2287          2296          2305          2314          2323
     CTC CGG GAT CCC CAC AGC CGG CGG CGA CAG CGG AGC CTG GGC CCA GAT GCA GAG
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      L   R   D   P   H   S   R   R   R   Q   R   S   L   G   P   D   A   E

          2332          2341          2350          2359          2368          2377
     CCT AGT TCT GTG CTG GCT TTC TGG AGG CTG ATC TGT GAC ACA TTC CGG AAG ATC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      P   S   S   V   L   A   F   W   R   L   I   C   D   T   F   R   K   I

          2386          2395          2404          2413          2422          2431
     GTA GAT AGC AAA TAC TTT GGC CGG GGA ATC ATG ATC GCC ATC CTG GTC AAT ACA
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      V   D   S   K   Y   F   G   R   G   I   M   I   A   I   L   V   N   T

          2440          2449          2458          2467          2476          2485
     CTC AGC ATG GGC ATC GAG TAC CAC GAG CAG CCC GAG GAG CTC ACC AAC GCC CTG
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      L   S   M   G   I   E   Y   H   E   Q   P   E   E   L   T   N   A   L

          2494          2503          2512          2521          2530          2539
     GAA ATC AGC AAC ATC GTC TTC ACC AGC CTC TTC GCC TTG GAG ATG CTG CTG AAA
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      E   I   S   N   I   V   F   T   S   L   F   A   L   E   M   L   L   K

          2548          2557          2566          2575          2584          2593
     CTG CTT GTC TAC GGT CCC TTT GGC TAC ATT AAG AAT CCC TAC AAC ATC TTT GAT
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      L   L   V   Y   G   P   F   G   Y   I   K   N   P   Y   N   I   F   D

          2602          2611          2620          2629          2638          2647
     GGT GTC ATT GTG GTC ATC AGT GTG TGG GAG ATT GTG GGC CAG CAG GGA GGT GGC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      G   V   I   V   V   I   S   V   W   E   I   V   G   Q   Q   G   G   G

          2656          2665          2674          2683          2692          2701
     CTG TCG GTG CTG CGG ACC TTC CGC CTG ATG CGG GTG CTG AAG CTG GTG CGC TTC
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      L   S   V   L   R   T   F   R   L   M   R   V   L   K   L   V   R   F

          2710          2719          2728          2737          2746          2755
     CTG CCG GCC CTG CAG CGC CAG CTC GTG GTG CTC ATG AAG ACC ATG GAC AAC GTG
     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
      L   P   A   L   Q   R   Q   L   V   V   L   M   K   T   M   D   N   V
```

DNASIS   DNA Translation [T-INS]

```
        2764          2773          2782          2791          2800          2809
GCC ACC TTC TGC ATG CTC CTC ATG CTG TTC ATC TTC ATC TTC AGC ATC CTG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   T   F   C   M   L   L   M   L   F   I   F   I   F   S   I   L   G

        2818          2827          2836          2845          2854          2863
ATG CAT CTC TTT GGT TGC AAG TTC GCA TCT GAA CGG GAT GGG GAC ACG TTG CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   H   L   F   G   C   K   F   A   S   E   R   D   G   D   T   L   P

        2872          2881          2890          2899          2908          2917
GAC CGG AAG AAT TTC GAC TCC CTG CTC TGG GCC ATC GTC ACT GTC TTT CAG ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   R   K   N   F   D   S   L   L   W   A   I   V   T   V   F   Q   I

        2926          2935          2944          2953          2962          2971
CTG ACT CAG GAA GAC TGG AAT AAA GTC CTC TAC AAC GGC ATG GCC TCC ACA TCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   T   Q   E   D   W   N   K   V   L   Y   N   G   M   A   S   T   S

        2980          2989          2998          3007          3016          3025
TCT TGG GCT GCT CTT TAC TTC ATC GCC CTC ATG ACT TTT GGC AAC TAT GTG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   W   A   A   L   Y   F   I   A   L   M   T   F   G   N   Y   V   L

        3034          3043          3052          3061          3070          3079
TTT AAC CTG CTG GTG GCC ATT CTT GTG GAA GGA TTC CAG GCA GAG GAA ATC GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   N   L   L   V   A   I   L   V   E   G   F   Q   A   E   E   I   G

        3088          3097          3106          3115          3124          3133
AAA CGG GAA GAT GCG AGT GGA CAG TTA AGC TGT ATT CAG CTG CCT GTC AAC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   R   E   D   A   S   G   Q   L   S   C   I   Q   L   P   V   N   S

        3142          3151          3160          3169          3178          3187
CAG GGG GGA GAT GCC ACC AAG TCT GAG TCA GAG CCT GAT TTC TTT TCG CCC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   G   G   D   A   T   K   S   E   S   E   P   D   F   F   S   P   S

        3196          3205          3214          3223          3232          3241
GTG GAT GGT GAT GGG GAC AGA AAG AAG CGC TTG GCC CTG GTG GCT TTG GGA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   D   G   D   G   D   R   K   K   R   L   A   L   V   A   L   G   E

        3250          3259          3268          3277          3286          3295
CAC GCG GAA CTA CGA AAG AGC CTT TTG CCA CCC CTC ATC ATC CAT ACG GCT GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   A   E   L   R   K   S   L   L   P   P   L   I   I   H   T   A   A

        3304          3313          3322          3331          3340          3349
ACA CCA ATG TCA CTA CCC AAG AGC TCC AGC ACA GGT GTG GGG GAA GCA CTG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   P   M   S   L   P   K   S   S   S   T   G   V   G   E   A   L   G

        3358          3367          3376          3385          3394          3403
TCT GGC TCT CGA CGT ACC AGT AGC AGT GGG TCC GCT GAG CCT GGA GCT GCC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   S   R   R   T   S   S   S   G   S   A   E   P   G   A   A   H

        3412          3421          3430          3439          3448          3457
CAT GAG ATG AAA TCT CCG CCA AGT GCC CGC AGC TCC CCG CAC AGT CCC TGG AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   E   M   K   S   P   P   S   A   R   S   S   P   H   S   P   W   S
```

DNASIS   DNA Translation [T-INS]

```
        3466      3475        3484        3493        3502        3511
GCG GCA AGC AGC TGG ACC AGC AGG CGC TCC AGC AGG AAC AGC CTG GGC CGG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   A   S   S   W   T   S   R   R   S   S   R   N   S   L   G   R   A

        3520      3529        3538        3547        3556        3565
CCC AGC CTA AAG CGG AGG AGC CCG AGC GGG GAG CGG AGG TCC CTG CTG TCT GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   S   L   K   R   R   S   P   S   G   E   R   R   S   L   L   S   G

        3574      3583        3592        3601        3610        3619
GAG GGC CAG GAG AGT CAG GAT GAG GAG GAA AGT TCA GAA GAG GAC CGG GCC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   Q   E   S   Q   D   E   E   S   E   D   R   A   S

        3628      3637        3646        3655        3664        3673
CCA GCA GGC AGT GAC CAT CGC CAC AGG GGT TCC TTG GAA CGT GAG GCC AAG AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   A   G   S   D   H   R   H   R   G   S   L   E   R   E   A   K   S

        3682      3691        3700        3709        3718        3727
TCC TTT GAC CTG CCT GAC ACT CTG CAG GTG CCG GGG CTG CAC CGC ACA GCC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   F   D   L   P   D   T   L   Q   V   P   G   L   H   R   T   A   S

        3736      3745        3754        3763        3772        3781
GGC CGG AGC TCT GCC TCT GAG CAC CAA GAC TGT AAT GGC AAG TCG GCT TCA GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   R   S   S   A   S   E   H   Q   D   C   N   G   K   S   A   S   G

        3790      3799        3808        3817        3826        3835
CGT TTG GCC CGC ACC CTG AGG ACT GAT GAC CCC CAA CTG GAT GGG GAT GAT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   L   A   R   T   L   R   T   D   D   P   Q   L   D   G   D   D   D

        3844      3853        3862        3871        3880        3889
AAT GAT GAG GGA AAT CTG AGC AAA GGG GAA CGC ATA CAA GCC TGG GTC AGA TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 N   D   E   G   N   L   S   K   G   E   R   I   Q   A   W   V   R   S

        3898      3907        3916        3925        3934        3943
CGG CTT CCT GCC TGT TGC CGA GAG CGA GAT TCC TGG TCG GCC TAT ATC TTT CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   L   P   A   C   C   R   E   R   D   S   W   S   A   Y   I   F   P

        3952      3961        3970        3979        3988        3997
CCT CAG TCA AGG TTT CGT CTC CTG TGT CAC CGG ATC ATC ACC CAC AAG ATG TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   Q   S   R   F   R   L   L   C   H   R   I   I   T   H   K   M   F

        4006      4015        4024        4033        4042        4051
GAC CAT GTG GTC CTC GTC ATC ATC TTC CTC AAC TGT ATC ACC ATC GCT ATG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   H   V   V   L   V   I   I   F   L   N   C   I   T   I   A   M   E

        4060      4069        4078        4087        4096        4105
CGC CCC AAA ATT GAC CCC CAC AGC GCT GAG CGC ATC TTC CTG ACC CTC TCC AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   P   K   I   D   P   H   S   A   E   R   I   F   L   T   L   S   N

        4114      4123        4132        4141        4150        4159
TAC ATC TTC ACG GCA GTC TTT CTA GCT GAA ATG ACA GTG AAG GTG GTG GCA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   I   F   T   A   V   F   L   A   E   M   T   V   K   V   V   A   L
```

DNASIS   DNA Translation [T-INS]

```
     4168         4177          4186          4195          4204          4213
GGC TGG TGC TTT GGG GAG CAG GCC TAC CTG CGC AGC AGC TGG AAT GTG CTG GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   W   C   F   G   E   Q   A   Y   L   R   S   S   W   N   V   L   D

     4222         4231          4240          4249          4258          4267
GGC TTG CTG GTG CTC ATC TCC GTC ATC GAC ATC CTG GTC TCC ATG GTC TCC GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   L   V   L   I   S   V   I   D   I   L   V   S   M   V   S   D

     4276         4285          4294          4303          4312          4321
AGC GGC ACC AAG ATC CTT GGC ATG CTG AGG GTG CTG CGG CTG CTG CGG ACC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   T   K   I   L   G   M   L   R   V   L   R   L   L   R   T   L

     4330         4339          4348          4357          4366          4375
CGT CCA CTC AGG GTC ATC AGC CGG GCC CAG GGA CTG AAG CTG GTG GTA GAG ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   P   L   R   V   I   S   R   A   Q   G   L   K   L   V   V   E   T

     4384         4393          4402          4411          4420          4429
CTG ATG TCA TCC CTC AAA CCC ATT GGC AAC ATT GTG GTC ATT TGC TGT GCC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   M   S   S   L   K   P   I   G   N   I   V   V   I   C   C   A   F

     4438         4447          4456          4465          4474          4483
TTC ATC ATT TTT GGA ATT CTC GGG GTG CAG CTC TTC AAA GGG AAG TTC TTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   I   I   F   G   I   L   G   V   Q   L   F   K   G   K   F   F   V

     4492         4501          4510          4519          4528          4537
TGT CAG GGT GAG GAC ACC AGG AAC ATC ACT AAC AAA TCC GAC TGC GCT GAG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   Q   G   E   D   T   R   N   I   T   N   K   S   D   C   A   E   A

     4546         4555          4564          4573          4582          4591
AGC TAC CGA TGG GTC CGG CAC AAG TAC AAC TTT GAC AAC CTG GGC CAG GCT CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Y   R   W   V   R   H   K   Y   N   F   D   N   L   G   Q   A   L

     4600         4609          4618          4627          4636          4645
ATG TCC CTG TTT GTG CTG GCC TCC AAG GAT GGT TGG GTT GAC ATC ATG TAT GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   S   L   F   V   L   A   S   K   D   C   W   V   D   I   M   Y   D

     4654         4663          4672          4681          4690          4699
GGG CTG GAT GCT GTG GGT GTG GAT CAG CAG CCC ATC ATG AAC CAC AAC CCC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   D   A   V   G   V   D   Q   Q   P   I   M   N   H   N   P   W

     4708         4717          4726          4735          4744          4753
ATG CTG CTA TAC TTC ATC TCC TTC CTC CTC ATC GTG GCC TTC TTT GTC CTG AAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   L   L   Y   F   I   S   F   L   L   I   V   A   F   F   V   L   N

     4762         4771          4780          4789          4798          4807
ATG TTT GTG GGC GTG GTG GTG GAG AAC TTC CAT AAG TGC AGA CAG CAC CAG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   F   V   G   V   V   V   E   N   F   H   K   C   R   Q   H   Q   E

     4816         4825          4834          4843          4852          4861
GAG GAG GAG GCG AGG CGG CGT GAG GAG AAG CGA CTA CGG AGG CTG GAG AAA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   E   A   R   R   R   E   E   K   R   L   R   R   L   E   K   K
```

DNASIS DNA Translation [T-INS]

```
      4870          4879          4888          4897          4906          4915
AGA AGG AAT CTA ATG TTG GAC GAT GTA ATT GCT TCC GGC AGC TCA GCC AGC GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   R   N   L   M   L   D   D   V   I   A   S   G   S   S   A   S   A

      4924          4933          4942          4951          4960          4969
GCG TCA GAA GCC CAG TGC AAG CCC TAC TAC TCT GAC TAC TCG AGA TTC CGG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   S   E   A   Q   C   K   P   Y   Y   S   D   Y   S   R   F   R   L

      4978          4987          4996          5005          5014          5023
CTT GTC CAC CAC CTG TGT ACC AGC CAC TAC CTG GAC CTC TTC ATC ACT GGT GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   V   H   H   L   C   T   S   H   Y   L   D   L   F   I   T   G   V

      5032          5041          5050          5059          5068          5077
ATC GGG CTG AAC GTG GTC ACT ATG GCC ATG GAA CAT TAC CAG CAG CCC CAG ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   G   L   N   V   V   T   M   A   M   E   H   Y   Q   Q   P   Q   I

      5086          5095          5104          5113          5122          5131
CTG GAC GAG GCT CTG AAG ATG TGC AAT TAC ATC TTT ACC GTC ATC TTT GTC TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   D   E   A   L   K   I   C   N   Y   I   F   T   V   I   F   V   F

      5140          5149          5158          5167          5176          5185
GAG TCA GTT TTC AAA CTT GTG GGC TTT GGC TTC CGC CGT TTC TTC CAG GAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   S   V   F   K   L   V   A   F   G   F   R   R   F   F   Q   D   R

      5194          5203          5212          5221          5230          5239
TGG AAC CAG CTG GAC CTG GCT ATT GTG CTT CTG TCC ATC ATG GGC ATC ACA CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   N   Q   L   D   L   A   I   V   L   L   S   I   M   G   I   T   L

      5248          5257          5266          5275          5284          5293
GAG GAG ATT GAG GTC AAT GCT TCG CTG CCC ATC AAC CCC ACC ATC ATC CGT ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   I   E   V   N   A   S   L   P   I   N   P   T   I   I   R   I

      5302          5311          5320          5329          5338          5347
ATG AGG GTG CTC CGC ATT GCT CGA GTT CTG AAG CTG TTG AAG ATG GCT GTG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   R   V   L   R   I   A   R   V   L   K   L   L   K   M   A   V   G

      5356          5365          5374          5383          5392          5401
ATG CGG GCA CTG CTG GAC ACG GTG ATG CAG GCC CTG CCC CAG GTG GGG AAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   R   A   L   L   D   T   V   M   Q   A   L   P   Q   V   G   N   L

      5410          5419          5428          5437          5446          5455
GGA CTT CTC TTC ATG TTA TTG TTT TTC ATC TTT CCA GCT CTG GGC GTG GAG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   L   L   F   M   L   L   F   F   I   F   A   A   L   G   V   E   L

      5464          5473          5482          5491          5500          5509
TTT GGA GAC CTG GAG TGT GAT GAG ACA CAC CCT TGT GAG GGC TTG GGT CGG CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   G   D   L   E   C   D   E   T   H   P   C   E   G   L   G   R   H

      5518          5527          5536          5545          5554          5563
GCC ACC TTT AGG AAC TTT GGT ATG GCC TTT CTG ACC CTC TTC CGA GTC TCC ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   T   F   R   N   F   G   M   A   F   L   T   L   F   R   V   S   T
```

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DNASIS   DNA Translation [T-INS]

```
      5572         5581         5590         5599         5608         5617
GGT GAC AAC TGG AAT GGT ATT ATG AAG GAC ACC CTC CGG GAC TGT GAC CAG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   D   N   W   N   G   I   M   K   D   T   L   R   D   C   D   Q   E

      5626         5635         5644         5653         5662         5671
TCC ACC TGC TAC AAC ACT GTC ATC TCC CCT ATC TAC TTT GTG TCC TTC GTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   T   C   Y   N   T   V   I   S   P   I   Y   F   V   S   F   V   L

      5680         5689         5698         5707         5716         5725
ACG GCC CAG TTT GTG CTG GTC AAC GTG GTC ATA GCT GTG CTG ATG AAG CAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   A   Q   F   V   L   V   N   V   V   I   A   V   L   M   K   H   L

      5734         5743         5752         5761         5770         5779
GAA GAA AGC AAC AAA GAG GCC AAG GAG GAG GCC GAG CTC GAG GCC GAG CTG GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   E   S   N   K   E   A   K   E   E   A   E   L   E   A   E   L   E

      5788         5797         5806         5815         5824         5833
CTG GAG ATG AAG ACG CTC AGC CTG CAG CCC CAC TCC CCG CTG GGC AGC CCC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   M   K   T   L   S   P   Q   P   H   S   P   L   G   S   P   F

      5842         5851         5860         5869         5878         5887
CTC TGG CCC GGG GTG GAG GGT GTC AAC AGT CCT GAC AGC CCT AAG CCT GGG GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   W   P   G   V   E   G   V   N   S   P   D   S   P   K   P   G   A

      5896         5905         5914         5923         5932         5941
CCA CAC ACC ACT GCC CAC ATT GGA GCA GCC TCG GGC TTC TCC CTT GAG CAC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   H   T   T   A   H   I   G   A   A   S   G   F   S   L   E   H   P

      5950         5959         5968         5977         5986         5995
ACG ATG GTA CCC CAC CCC GAG GAG GTG CCA GTC CCC CTA GGA CCA GAC CTG CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   M   V   P   H   P   E   E   V   P   V   P   L   G   P   D   L   L

      6004         6013         6022         6031         6040         6049
ACT GTG AGG AAG TCT GGT GTC AGC CGG ACG CAC TCT CTG CCC AAT GAC AGC TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   V   R   K   S   G   V   S   R   T   H   S   L   P   N   D   S   Y

      6058         6067         6076         6085         6094         6103
ATG TGC CGC AAT GGG AGC ACT GCT GAG AGA TCC CTA GGA CAC AGG GGC TGG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 M   C   R   N   G   S   T   A   E   R   S   L   G   H   R   G   W   G

      6112         6121         6130         6139         6148         6157
CTC CCC AAA GCC CAG TCA GGC TCC ATC TTG TCC GTT CAC TCC CAA CCA GCA GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   P   K   A   Q   S   G   S   I   L   S   V   H   S   Q   P   A   D

      6166         6175         6184         6193         6202         6211
ACC AGC TGC ATC CTA CAG CTT CCC AAA GAT GTG CAC TAT CTG CTC CAG CCT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 T   S   C   I   L   Q   L   P   K   D   V   H   Y   L   L   Q   P   H

      6220         6229         6238         6247         6256         6265
GGG GCC CCC ACC TGG GGC GCC ATC CCT AAA CTA CCC CCA CCT GGC CGC TCC CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   A   P   T   W   G   A   I   P   K   L   P   P   P   G   R   S   P
```

DNASIS   DNA Translation [T-INS]

```
        6274        6283        6292        6301        6310        6319
CTG GCT CAG AGG CCT CTC AGG CGC CAG GCA GCA ATA AGG ACT GAC TCC CTG GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   A   Q   R   P   L   R   R   Q   A   A   I   R   T   D   S   L   D

        6328        6337        6346        6355        6364        6373
GTG CAG GGC CTG GGT AGC CGG GAA GAC CTG TTG TCA GAG GTG AGT GGG CCC TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   Q   G   L   G   S   R   E   D   L   L   S   E   V   S   G   P   S

        6382        6391        6400        6409        6418        6427
TGC CCT CTG ACC CGG TCC TCA TCC TTC TGG GGC GGG TCG AGC ATC CAG GTG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   L   T   R   S   S   S   F   W   G   G   S   S   I   Q   V   Q

        6436        6445        6454        6463        6472        6481
CAG CGT TCC GGC ATC CAG AGC AAA GTC TCC AAG CAC ATC CGC CTG CCA GCC CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   R   S   G   I   Q   S   K   V   S   K   H   I   R   L   P   A   P

        6490        6499        6508        6517        6526        6535
TGC CCA GGC CTG GAA CCC AGC TGG GCC AAG GAC CCT CCA GAG ACC AGA AGC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   P   G   L   E   P   S   W   A   K   D   P   P   E   T   R   S   S

        6544        6553        6562        6571        6580        6589
TTA GAG CTG GAC ACG GAG CTG AGC TGG ATT TCA GGA GAC CTC CTT CCC AGC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   L   D   T   E   L   S   W   I   S   G   D   L   L   P   S   S

        6598        6607        6616        6625        6634        6643
CAG GAA GAA CCC CTG TCC CCA CGG GAC CTG AAG AAG TGC TAC AGT GTA GAG ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   E   E   P   L   S   P   R   D   L   K   K   C   Y   S   V   E   T

        6652        6661        6670        6679        6688        6697
CAG AGC TGC AGG CGC AGG CCT GGG TCC TGG CTA GAT GAA CAG CGG AGA CAC TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   S   C   R   R   R   P   G   S   W   L   D   E   Q   R   R   H   S

        6706        6715        6724        6733        6742        6751
ATT GCT GTC AGC TGT CTG GAC AGC GGC TCC CAA CCC CGC CTA TGT CCA AGC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   A   V   S   C   L   D   S   G   S   Q   P   R   L   C   P   S   P

        6760        6769        6778        6787        6796        6805
TCA AGC CTC GGG GGC CAA CCT CTT GGG GGT CCT GGG AGC CGG CCT AAG AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   S   L   G   G   Q   P   L   G   G   P   G   S   R   P   K   K   K

        6814        6823        6832        6841        6850        6859
CTC AGC CCA CCC AGT ATC TCT ATA GAC CCC CCG GAG AGC CAG GGC TCT CGG CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   S   P   P   S   I   S   I   D   P   P   E   S   Q   G   S   R   P

        6868        6877        6886        6895        6904        6913
CCA TGC AGT CCT GGT GTC TGC CTC AGG AGG AGG GCG CCG GCC AGT GAC TCT AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   C   S   P   G   V   C   L   R   R   R   A   R   A   S   D   S   K

        6922        6931        6940        6949        6958        6967
GAT CCC TCG GTC TCC AGC CCC CTT GAC AGC ACG GCT GCC TCA CCC TCC CCA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   P   S   V   S   S   P   L   D   S   T   A   A   S   P   S   P   K
```

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DNASIS   DNA Translation [T-INS]

```
        6976          6985           6994          7003          7012          7021
AAA GAC ACG CTG AGT CTC TCT GGT TTG TCT TCT GAC CCA ACA GAC ATG GAC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   D   T   L   S   L   S   G   L   S   S   D   P   T   D   M   D   P

        7030          7039           7048          7057          7066          7075
TGA GTC CTA CCC ACT CTC CCC CAT CAC CTT TCT CCA CCG GGT GCA GAT CCT AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 *   V   L   P   T   L   P   H   H   L   S   P   P   G   A   D   P   S

        7084          7093           7102          7111          7120          7129
TCC GCC TCC TGG GCA GCG TTT CTG AAA AGT CCC ACG TAA GCA GCA AGC AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   A   S   W   A   A   F   L   K   S   P   T   *   A   A   S   S   H

        7138          7147           7156          7165          7174          7183
GAG GCA CCT CAC CTG CCT TCT TCA GTG GCT GGT GGG GAT GAC GAG CAG AAC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   A   P   H   L   P   S   S   V   A   G   G   D   D   E   Q   N   F

        7192          7201           7210          7219          7228          7237
CGG AGA GTC GAT CTG AAG AGA ACA CAG CCC TGG AGC CCC TGC CTC CGG GAA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   R   V   D   L   K   R   T   Q   P   W   S   P   C   L   R   E   E

        7246          7255           7264          7273          7282
GGA AAA GGA GAA AGC CCA GTG TGG CCA AGG CTC CCG ACA CCA GGA GCT G/3'      SEQ 1 + 3
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   K   G   E   S   P   V   W   P   R   L   P   T   P   G   A/       SEQ 2 + 4
```

DNASIS
T-INS
SEQ ID NO:3

start of
SEQ ID NO:1
coding region

```
         10         20         30         40         50         60
GGAGCTGAGC TGAACTGGCC CTCCTGGGGA CTCAGCAAGC TCTCTAGAGC CCCCCACATG

         70         80         90        100        110        120
CTCCCCCACC GGGGTCCCCC GGTTGCGTGA GGACACCTCC TCTGAGGGGC TCCGCTCGCC

        130        140        150        160        170        180
CCTCTTCGGA CCCCCCGGGG CCCCGGCTGG CCAGAGGATG GACGAGGAGG AGGATGGAGC

        190        200        210        220        230        240
GGGCGCCGAG GAGTCGGGAC AGCCCCGTAG CTTCACGCAG CTCAACGACC TGTCCGGGGC

        250        260        270        280        290        300
CGGGGGCCGG CAGGGGCCGG GGTCGACGGA AAAGGACCCG GGCAGCGCGG ACTCCGAGGC

        310        320        330        340        350        360
GGAGGGGCTG CCGTACCCGG CGCTAGCCCC GGTGGTTTTC TTCTACTTGA GCCAGGACAG

        370        380        390        400        410        420
CCGCCCGCGG AGCTGGTGTC TCCGCACGGT CTGTAACCCG TGGTTCGAGC GAGTCAGTAT

        430        440        450        460        470        480
GCTGGTCATT CTTCTCAACT GTGTGACTCT GGGTATGTTC AGGCCGTGTG AGGACATTGC

        490        500        510        520        530        540
CTGTGACTCC CAGCGCTGCC GGATCCTGCA GGCCTTCGAT GACTTCATCT TTGCCTTCTT

        550        560        570        580        590        600
TGCTGTGGAA ATGGTGGTGA AGATGGTGGC CTTGGGCATC TTTGGGAAGA AATGTTACCT

        610        620        630        640        650        660
GGGAGACACT TGGAACCGGC TTGACTTTTT CATTGTCATT GCAGGGATGC TGGAGTATTC

        670        680        690        700        710        720
GCTGGACCTG CAGAACGTCA GCTTCTCCGC AGTCAGGACA GTCCGTGTGC TGCGACCGCT

        730        740        750        760        770        780
CAGGGCCATT AACCGGGTGC CCAGCATGCG CATTCTCGTC ACATTACTGC TGGACACCTT

        790        800        810        820        830        840
GCCTATGCTG GGCAACGTCC TGCTGCTCTG TTTGTTCGTC TTTTTCATCT TTGGCATCGT

        850        860        870        880        890        900
GGGCGTCCAG CTGTGGGCAG GACTGCTTCG CAACCGATGC TTCCTCCCCG AGAACTTCAG

        910        920        930        940        950        960
CCTCCCCCTG AGCGTGGACC TGGAGCCTTA TTACCAGACA GAGAATGAGG ACGAGAGCCC

        970        980        990       1000       1010       1020
CTTCATCTGC TCTCAGCCTC GGGAGAATGG CATGAGATCG TGCAGGAGTG TGCCCACACT

       1030       1040       1050       1060       1070       1080
GCGTGGGGAA GGCGGTGGTG GCCCACCCTG CAGTCTGGAC TATGAGACCT ATAACAGTTC

       1090       1100       1110       1120       1130       1140
CAGCAACACC ACCTGTGTCA ACTGGAACCA GTACTATACC AACTGCTCTG CGGGCGAGCA

       1150       1160       1170       1180       1190       1200
CAACCCCTTC AAAGGCGCCA TCAACTTTGA CAACATTGGC TATGCCTGGA TCGCCATCTT

       1210       1220       1230       1240       1250       1260
CCAGGTCATC ACACTGGAGG GCTGGGTCGA CATCATGTAC TTCGTAATGG ACGCTCACTC
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DNASIS
T-INS

```
         1270       1280       1290       1300       1310       1320
CTTCTACAAC TTCATCTACT TCATTCTTCT CATCATCGTG GGCTCCTTCT TCATGATCAA

         1330       1340       1350       1360       1370       1380
CCTGTGCCTG GTGGTGATTG CCACGCAGTT CTCCGAGACC AAACAGCGGG AGAGTCAGCT

         1390       1400       1410       1420       1430       1440
GATGCGGGAG CAGCGTGTAC GATTCCTGTC CAATGCTAGC ACCCTGGCAA GCTTCTCTGA

         1450       1460       1470       1480       1490       1500
GCCAGGCAGC TGCTATGAGG AGCTACTCAA GTACCTGGTG TACATCCTCC GAAAAGCAGC

         1510       1520       1530       1540       1550       1560
CCGAAGGCTG GCCCAGGTCT CTAGGGCTAT AGGCGTGCGG GCTGGGCTGC TCAGCAGCCC

         1570       1580       1590       1600       1610       1620
AGTGGCCCGT AGTGGGCAGG AGCCCCAGCC CAGTGGCAGC TGCACTCGCT CACACCGTCG

         1630       1640       1650       1660       1670       1680
TCTGTCTGTC CACCACCTGG TCCACCACCA TCACCACCAC CATCACCACT ACCACCTGGG

         1690       1700       1710       1720       1730       1740
TAATGGGACG CTCAGAGTTC CCCGGGCCAG CCCAGAGATC CAGGACAGGG ATGCCAATGG

         1750       1760       1770       1780       1790       1800
GTCTCGCCGG CTCATGCTAC CACCACCCTC TACACCCACT CCCTCTGGGG GCCCTCCGAG

         1810       1820       1830       1840       1850       1860
GGGTGCGGAG TCTGTACACA GCTTCTACCA TGCTGACTGC CACTTGGAGC CAGTCCGTTG

         1870       1880       1890       1900       1910       1920
CCAGGCACCC CCTCCCAGAT GCCCATCGGA GGCATCTGGT AGGACTGTGG GTAGTGGGAA

         1930       1940       1950       1960       1970       1980
GGTGTACCCC ACTGTGCATA CCAGCCCTCC ACCAGAGATA CTGAAGGATA AAGCACTAGT

         1990       2000       2010       2020       2030       2040
GGAGGTGGCC CCCAGCCCTG GGCCCCCCAC CCTCACCAGC TTCAACATCC CACCTGGGCC

         2050       2060       2070       2080       2090       2100
CTTCAGCTCC ATGCACAAGC TCCTGGAGAC ACAGAGTACG GGAGCCTGCC ATAGCTCCTG

         2110       2120       2130       2140       2150       2160
CAAAATCTCC AGCCCTTGCT CCAAGGCAGA CAGTGGAGCC TGCGGGCCGG ACAGTTGTCC

         2170       2180       2190       2200       2210       2220
CTACTGTGCC CGGACAGGAG CAGGAGAGCC AGAGTCCGCT GACCATGTCA TGCCTGACTC

         2230       2240       2250       2260       2270       2280
AGACAGCGAG GCTGTGTATG AGTTCACACA GGACGCTCAG CACAGTGACC TCCGGGATCC

         2290       2300       2310       2320       2330       2340
CCACAGCCGG CGGCGACAGC GGAGCCTGGG CCCAGATGCA GAGCCTAGTT CTGTGCTGGC

         2350       2360       2370       2380       2390       2400
TTTCTGGAGG CTGATCTGTG ACACATTCCG GAAGATCGTA GATAGCAAAT ACTTTGGCCG

         2410       2420       2430       2440       2450       2460
GGGAATCATG ATCGCCATCC TGGTCAATAC ACTCAGCATG GGCATCGAGT ACCACGAGCA

         2470       2480       2490       2500       2510       2520
GCCCGAGGAG CTCACCAACG CCCTGGAAAT CAGCAACATC GTCTTCACCA GCCTCTTCGC
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DNASIS
T-INS

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        2530       2540       2550       2560       2570       2580
CTTGGAGATG CTGCTGAAAC TGCTTGTCTA CGGTCCCTTT GGCTACATTA AGAATCCCTA

        2590       2600       2610       2620       2630       2640
CAACATCTTT GATGGTGTCA TTGTGGTCAT CAGTGTGTGG GAGATTGTGG GCCAGCAGGG

        2650       2660       2670       2680       2690       2700
AGGTGGCCTG TCGGTGCTGC GGACCTTCCG CCTGATGCGG GTGCTGAAGC TGGTGCGCTT

        2710       2720       2730       2740       2750       2760
CCTGCCGGCC CTGCAGCGCC AGCTCGTGGT GCTCATGAAG ACCATGGACA ACGTGGCCAC

        2770       2780       2790       2800       2810       2820
CTTCTGCATG CTCCTCATGC TGTTCATCTT CATCTTCAGC ATCCTGGGCA TGCATCTCTT

        2830       2840       2850       2860       2870       2880
TGGTTGCAAG TTCGCATCTG AACGGGATGG GGACACGTTG CCAGACCGGA AGAATTTCGA

        2890       2900       2910       2920       2930       2940
CTCCCTGCTC TGGGCCATCG TCACTGTCTT TCAGATTCTG ACTCAGGAAG ACTGGAATAA

        2950       2960       2970       2980       2990       3000
AGTCCTCTAC AACGGCATGG CCTCCACATC GTCTTGGGCT GCTCTTTACT TCATCGCCCT

        3010       3020       3030       3040       3050       3060
CATGACTTTT GGCAACTATG TGCTGTTTAA CCTGCTGGTG GCCATTCTTG TGGAAGGATT

        3070       3080       3090       3100       3110       3120
CCAGGCAGAG GAAATCGGCA AACGGGAAGA TGCGAGTGGA CAGTTAAGCT GTATTCAGCT

        3130       3140       3150       3160       3170       3180
GCCTGTCAAC TCTCAGGGGG GAGATGCCAC CAAGTCTGAG TCAGAGCCTG ATTTCTTTTC

        3190       3200       3210       3220       3230       3240
GCCCAGTGTG GATGGTGATG GGGACAGAAA GAAGCGCTTG GCCCTGGTGG CTTTGGGAGA

        3250       3260       3270       3280       3290       3300
ACACGCGGAA CTACGAAAGA GCCTTTTGCC ACCCTCATC ATCCATACGG CTGCGACACC

        3310       3320       3330       3340       3350       3360
AATGTCACTA CCCAAGAGCT CCAGCACAGG TGTGGGGAA GCACTGGGCT CTGGCTCTCG

        3370       3380       3390       3400       3410       3420
ACGTACCAGT AGCAGTGGGT CCGCTGAGCC TGGAGCTGCC CACCATGAGA TGAAATCTCC

        3430       3440       3450       3460       3470       3480
GCCAAGTGCC CGCAGCTCCC CGCACAGTCC CTGGAGTGCG GCAAGCAGCT GGACCAGCAG

        3490       3500       3510       3520       3530       3540
GCGCTCCAGC AGGAACAGCC TGGGCCGGGC CCCCAGCCTA AAGCGGAGGA GCCCGAGCGG

        3550       3560       3570       3580       3590       3600
GGAGCGGAGG TCCCTGCTGT CTGGAGAGGG CCAGGAGAGT CAGGATGAGG AGGAAAGTTC

        3610       3620       3630       3640       3650       3660
AGAAGAGGAC CGGGCCAGCC CAGCAGGCAG TGACCATCGC CACAGGGGTT CCTTGGAACG

        3670       3680       3690       3700       3710       3720
TGAGGCCAAG AGTTCCTTTG ACCTGCCTGA CACTCTGCAG GTGCCGGGGC TGCACCGCAC

     3730          3740       3750       3760       3770       3780
AGCCAGCGGC CGGAGCTCTG CCTCTGAGCA CCAAGACTGT AATGGCAAGT CGGCTTCAGG
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DNASIS
T-INS

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         3790        3800        3810        3820        3830        3840
    GCGTTTGGCC CGCACCCTGA GGACTGATGA CCCCCAACTG GATGGGGATG ATGACAATGA

         3850        3860        3870        3880        3890        3900
    TGAGGGAAAT CTGAGCAAAG GGGAACGCAT ACAAGCCTGG GTCAGATCCC GGCTTCCTGC

         3910        3920        3930        3940        3950        3960
    CTGTTGCCGA GAGCGAGATT CCTGGTCGGC CTATATCTTT CCTCCTCAGT CAAGGTTTCG

         3970        3980        3990        4000        4010        4020
    TCTCCTGTGT CACCGGATCA TCACCCACAA GATGTTTGAC CATGTGGTCC TCGTCATCAT

         4030        4040        4050        4060        4070        4080
    CTTCCTCAAC TGTATCACCA TCGCTATGGA GCGCCCCAAA ATTGACCCCC ACAGCGCTGA

         4090        4100        4110        4120        4130        4140
    GCGCATCTTC CTGACCCTCT CCAACTACAT CTTCACGGCA GTCTTTCTAG CTGAAATGAC

         4150        4160        4170        4180        4190        4200
    AGTGAAGGTG GTGGCACTGG GCTGGTGCTT TGGGGAGCAG GCCTACCTGC GCAGCAGCTG

         4210        4220        4230        4240        4250        4260
    GAATGTGCTG GACGGCTTGC TGGTGCTCAT CTCCGTCATC GACATCCTGG TCTCCATGGT

         4270        4280        4290        4300        4310        4320
    CTCCGACAGC GGCACCAAGA TCCTTGGCAT GCTGAGGGTG CTGCGGCTGC TGCGGACCCT

         4330        4340        4350        4360        4370        4380
    GCGTCCACTC AGGGTCATCA GCCGGGCCCA GGGACTGAAG CTGGTGGTAG AGACTCTGAT

         4390        4400        4410        4420        4430        4440
    GTCATCCCTC AAACCCATTG GCAACATTGT GGTCATTTGC TGTGCCTTCT TCATCATTTT

         4450        4460        4470        4480        4490        4500
    TGGAATTCTC GGGGTGCAGC TCTTCAAAGG GAAGTTCTTC GTGTGTCAGG GTGAGGACAC

         4510        4520        4530        4540        4550        4560
    CAGGAACATC ACTAACAAAT CCGACTGCGC TGAGGCCAGC TACCGATGGG TCCGGCACAA

         4570        4580        4590        4600        4610        4620
    GTACAACTTT GACAACCTGG GCCAGGCTCT GATGTCCCTG TTTGTGCTGG CCTCCAAGGA

         4630        4640        4650        4660        4670        4680
    TGGTTGGGTT GACATCATGT ATGATGGGCT GGATGCTGTG GGTGTGGATC AGCAGCCCAT

         4690        4700        4710        4720        4730        4740
    CATGAACCAC AACCCCTGGA TGCTGCTATA CTTCATCTCC TTCCTCCTCA TCGTGGCCTT

         4750        4760        4770        4780        4790        4800
    CTTTGTCCTG AACATGTTTG TGGGCGTGGT GGTGGAGAAC TTCCATAAGT GCAGACAGCA

         4810        4820        4830        4840        4850        4860
    CCAGGAGGAG GAGGAGGCGA GGCGGCGTGA GGAGAAGCGA CTACGGAGGC TGGAGAAAAA

         4870        4880        4890        4900        4910        4920
    GAGAAGGAAT CTAATGTTGG ACGATGTAAT TGCTTCCGGC AGCTCAGCCA GCGCTGCGTC

         4930        4940        4950        4960        4970        4980
    AGAAGCCCAG TGCAAGCCCT ACTACTCTGA CTACTCGAGA TTCCGGCTCC TTGTCCACCA

         4990        5000        5010        5020        5030        5040
    CCTGTGTACC AGCCACTACC TGGACCTCTT CATCACTGGT GTCATCGGGC TGAACGTGGT
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DNASIS
T-INS

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      5050       5060       5070       5080       5090       5100
CACTATGGCC ATGGAACATT ACCAGCAGCC CCAGATCCTG GACGAGGCTC TGAAGATCTG

      5110       5120       5130       5140       5150       5160
CAATTACATC TTTACCGTCA TCTTTGTCTT TGAGTCAGTT TTCAAACTTG TGGCCTTTGG

      5170       5180       5190       5200       5210       5220
CTTCCGCCGT TTCTTCCAGG ACAGGTGGAA CCAGCTGGAC CTGGCTATTG TGCTTCTGTC

      5230       5240       5250       5260       5270       5280
CATCATGGGC ATCACACTGG AGGAGATTGA GGTCAATGCT TCGCTGCCCA TCAACCCCAC

      5290       5300       5310       5320       5330       5340
CATCATCCGT ATCATGAGGG TGCTCCGCAT TGCTCGAGTT CTGAAGCTGT TGAAGATGGC

      5350       5360       5370       5380       5390       5400
TGTGGGCATG CGGGCACTGC TGGACACGGT GATGCAGGCC CTGCCCCAGG TGGGGAACCT

      5410       5420       5430       5440       5450       5460
GGGACTTCTC TTCATGTTAT TGTTTTTCAT CTTTGCAGCT CTGGGCGTGG AGCTCTTTGG

      5470       5480       5490       5500       5510       5520
AGACCTGGAG TGTGATGAGA CACACCCTTG TGAGGGCTTG GGTCGGCATG CCACCTTTAG

      5530       5540       5550       5560       5570       5580
GAACTTTGGT ATGGCCTTTC TGACCCTCTT CCGAGTCTCC ACTGGTGACA ACTGGAATGG

      5590       5600       5610       5620       5630       5640
TATTATGAAG GACACCCTCC GGGACTGTGA CCAGGAGTCC ACCTGCTACA ACACTGTCAT

      5650       5660       5670       5680       5690       5700
CTCCCCTATC TACTTTGTGT CCTTCGTGCT GACGGCCCAG TTTGTGCTGG TCAACGTGGT

      5710       5720       5730       5740       5750       5760
CATAGCTGTG CTGATGAAGC ACCTGGAAGA AAGCAACAAA GAGGCCAAGG AGGAGGCCGA

      5770       5780       5790       5800       5810       5820
GCTCGAGGCC GAGCTGGAGC TGGAGATGAA GACGCTCAGC CCGCAGCCCC ACTCCCCGCT

      5830       5840       5850       5860       5870       5880
GGGCAGCCCC TTCCTCTGGC CCGGGGTGGA GGGTGTCAAC AGTCCTGACA GCCCTAAGCC

      5890       5900       5910       5920       5930       5940
TGGGGCTCCA CACACCACTG CCCACATTGG AGCAGCCTCG GGCTTCTCCC TTGAGCACCC

      5950       5960       5970       5980       5990       6000
CACGATGGTA CCCCACCCCG AGGAGGTGCC AGTCCCCCTA GGACCAGACC TGCTGACTGT

      6010       6020       6030       6040       6050       6060
GAGGAAGTCT GGTGTCAGCC GGACGCACTC TCTGCCCAAT GACAGCTACA TGTGCCGCAA

      6070       6080       6090       6100       6110       6120
TGGGAGCACT GCTGAGAGAT CCCTAGGACA CAGGGGCTGG GGGCTCCCCA AAGCCCAGTC

      6130       6140       6150       6160       6170       6180
AGGCTCCATC TTGTCCGTTC ACTCCCAACC AGCAGACACC AGCTGCATCC TACAGCTTCC

      6190       6200       6210       6220       6230       6240
CAAAGATGTG CACTATCTGC TCCAGCCTCA TGGGGCCCCC ACCTGGGGCG CCATCCCTAA

      6250       6260       6270       6280       6290       6300
ACTACCCCCA CCTGGCCGCT CCCCTCTGGC TCAGAGGCCT CTCAGGCGCC AGGCAGCAAT
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DNASIS
T-INS

        6310        6320        6330        6340        6350        6360
AAGGACTGAC TCCCTGGATG TGCAGGGCCT GGGTAGCCGG GAAGACCTGT TGTCAGAGGT

        6370        6380        6390        6400        6410        6420
GAGTGGGCCC TCCTGCCCTC TGACCCGGTC CTCATCCTTC TGGGGCGGGT CGAGCATCCA

        6430        6440        6450        6460        6470        6480
GGTGCAGCAG CGTTCCGGCA TCCAGAGCAA AGTCTCCAAG CACATCCGCC TGCCAGCCCC

        6490        6500        6510        6520        6530        6540
TTGCCCAGGC CTGGAACCCA GCTGGGCCAA GGACCCTCCA GAGACCAGAA GCAGCTTAGA

        6550        6560        6570        6580        6590        6600
GCTGGACACG GAGCTGAGCT GGATTTCAGG AGACCTCCTT CCCAGCAGCC AGGAAGAACC

        6610        6620        6630        6640        6650        6660
CCTGTCCCCA CGGGACCTGA AGAAGTGCTA CAGTGTAGAG ACCCAGAGCT GCAGGCGCAG

        6670        6680        6690        6700        6710        6720
GCCTGGGTCC TGGCTAGATG AACAGCGGAG ACACTCCATT GCTGTCAGCT GTCTGGACAG

        6730        6740        6750        6760        6770        6780
CGGCTCCCAA CCCCGCCTAT GTCCAAGCCC CTCAAGCCTC GGGGGCCAAC CTCTTGGGGG

        6790        6800        6810        6820        6830        6840
TCCTGGGAGC CGGCCTAAGA AAAACTCAG CCCACCCAGT ATCTCTATAG ACCCCCCGGA

        6850        6860        6870        6880        6890        6900
GAGCCAGGGC TCTCGGCCCC CATGCAGTCC TGGTGTCTGC CTCAGGAGGA GGGCGCCGGC

        6910        6920        6930        6940        6950        6960
CAGTGACTCT AAGGATCCCT CGGTCTCCAG CCCCCTTGAC AGCACGGCTG CCTCACCCTC

        6970        6980        6990        7000        7010        7020
CCCAAAGAAA GACACGCTGA GTCTCTCTGG TTTGTCTTCT GACCCAACAG ACATGGACCC

        7030        7040        7050        7060        7070        7080
CTGAGTCCTA CCCACTCTCC CCCATCACCT TTCTCCACCG GGTGCAGATC CTAGCTCCGC

        7090        7100        7110        7120        7130        7140
CTCCTGGGCA GCGTTTCTGA AAAGTCCCAC GTAAGCAGCA AGCAGCCACG AGGCACCTCA

        7150        7160        7170        7180        7190        7200
CCTGCCTTCT TCAGTGGCTG GTGGGGATGA CGAGCAGAAC TTCCGGAGAG TCGATCTGAA

        7210        7220        7230        7240        7250        7260
GAGAACACAG CCCTGGAGCC CCTGCCTCCG GGAAGAAGGA AAAGGAGAAA GCCCAGTGTG

        7270        7280        7290        7300        7310        7320
GCCAAGGCTC CCGACACCAG GAGCTG ...  .........  .........  .........
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ELS*TGPPGDSASSLEPPTCSPTGVPRLREDTSSEGLRSPLFGPPG
APAGQR■DEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEK
DPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFE
RVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAV
EMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVS
FSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFV
FFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDES
PFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTT
CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV
DIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQR
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VHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPST
PTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTV
GSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSS
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EPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA
EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ
PEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVI
VVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLM
KTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRK
NFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMT
FGNYVLFNLLVAILVEGFQAEEIGKREDASGQLSCIQLPVNSQGGD
ATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLII
HTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKS
PPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS
LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPD
TLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDG
DDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFR
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YIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVI
DILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETL
MSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK
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DAVGVDQQPIMNHNPWMLLYFISRLLIVAFFVLNMFVGVVVENFH
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EAQCKPYYSDYSRFRLLVHHLCTSRYLDLFITGVIGLNVVTMAME
HYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQ
LDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKM
AVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLEC
DETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC
DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA
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TSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQA
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DLLPSSQEEPLSPRDLKKCYSVETQSCRRRPGSWLDEQRRHSIAV
SCLDSGSQPRLCPSPSSLGGQPLGPGSRRKKKLSPPSISIDPPESQ
GSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSL
SGLSSDPTDMDP*VLPTLPHHLSPPGADPSSASWAAFLKSPT*AAS
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SPVWPRLPTPGA
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SEQ ID NO:5:   SKEKQMA

SEQ ID NO:6: 5'TNGC(A/C/T)ATGGAG(C/A)GNCC(C/T)-3'

SEQ ID NO:7: 5'-CTT(C/G/T)CCCTTGAA(G/C)A(G/A)CTG)-3'

SEQ ID NO:8: 5'-CCGCTGTCGGAGACCATGGAGACC-3'

SEQ ID NO:9: 5'-AGCGGCCCAAAATTGACCCCCACAG-3'

SEQ ID NO:10: 5'-GAAGATGCGAGTGGACAG-3'

SEQ ID NO:11: 5'- CTGTGGCGATGGTCACTG-3'